REMARKS

Applicants kindly thank the Examiner for the productive interview conducted at the USPTO on July 18, 2002. Favorable reconsideration of the subject application is respectfully requested in view of the following remarks. With the above amendement, claim 80 has been canceled and rewritten as independent claims 85-89. Claims 6, 81 and 82 have been amended. Thus, with this amendment, claims 6 and 81-89 are pending. It is urged that support for the amendments may be found throughout the specification as originally filed and that none of the amendments constitutes new matter. Specifically, support for open reading frame can be found, for example, on page 122, lines 14 – 18. Claims 81 and 82 were amended solely to remove reference to cancelled claim 80 and to add dependency to the newly rewritten claims 85-89. It should also be noted that the above amendments are made without prejudice to prosecution of any or all subject matter modified and/or removed by this amendment in a related divisional, continuation and/or continuation-in-part application.

Rejections under 35 U.S.C. § 112, first paragraph (written description)

Claims 6 and 80-84 are rejected as allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Examiner acknowledges that Applicants have provided sufficient descriptive information to demonstrate that Applicants were in possession of the claimed invention as per the guidelines for "Written Description". However, the Examiner believes that the amendments to the claims do not find adequate support in the specification as filed. In particular, as discussed at the interview conducted on July 18, 2002, the Examiner alleges that "at least the coding region of a sequence" is not adequately described in that it could potentially read on a full chromosome. Further, the Examiner believes that the disclosure does not show that the sequence of SEQ ID NO:474 is over expressed in breast tissue as compared to normal tissue and therefore the functional limitation recited in the claims is allegedly not supported.

Applicants respectfully traverse this rejection on the following grounds. Applicants submit that the claims as amended recite an isolated polynucleotide **useful in the detection of breast cancer**, comprising a sequence selected from the group consisting of (a) complements of the sequence provided in SEQ ID NO:474; (b) sequences consisting of at least 20 contiguous nucleotides of a sequence provided in SEQ ID NO:474; (c) sequences that hybridize to a sequence provided in SEQ ID NO:474, under moderately stringent conditions; (d) sequences having at least 90% identity to a sequence of SEQ ID NO:474; and (e) degenerate variants of a sequence provided in SEQ ID NO:474 (emphasis added). Applicants submit that the skilled artisan would readily recognize in light of the instant disclosure, that Applicants have more than adequately demonstrated that SEQ ID NO:474 can be used in the detection of breast cancer. In particular, the specification clearly teaches that the cDNA sequence of SEQ ID NO:71 is over expressed in breast tumor tissue as compared to normal tissues. The specification also teaches that SEQ ID NO:71 is a partial cDNA sequence of B726P, which has numerous isoforms, one of which is set forth in SEQ ID NO:474 (see page 122, lines 5 – 18). Further, the skilled artisan would readily recognize upon alignment of these sequences using any of a variety of art-recognized sequence alignment programs, that SEQ ID NO:71 substantially overlaps with SEQ ID NO:474. Thus, the skilled artisan would readily appreciate that there is a reasonable expectation that SEQ ID NO:474 is expressed in the same tumor-associated manner as was demonstrated by Applicants for the partial cDNA sequence of SEQ ID NO:71. Further still, as discussed during the interview conducted on July 18, 2002, Applicants attach herewith the Declaration of Susan Harlocker, Ph.D., describing mRNA expression analysis of B726P combined ORF (SEQ ID NO:474) using real-time PCR in a panel of breast tumor and normal tissue samples. These results clearly confirm, as described in the Applicants specification as filed, and as would be expected by the skilled artisan in view of the Applicants' original disclosure, that the polynucleotide set forth in SEQ ID NO:474 is expressed in breast tumor tissue but is not expressed in normal breast tissue.

Additionally, the specification clearly describes numerous assays that can be used for the detection of breast cancer using the polynucleotides of the present invention, for

example on page 115, line 25 – page 117, line 2. Thus, Applicants urge that the skilled artisan would readily recognize, in light of the Applicants' disclosure, an illustrative single identifying characteristic common to the claimed polynucleotides, *i.e.*, the ability to be used in the detection of breast cancer.

Moreover, in view of this identifying characteristic, the skilled artisan would immediately recognize that the Applicants were in possession of much more than the specifically recited species of SEQ ID NO:474. In view of the tumor-specific expression profile identified by the Applicants for this sequence, the skilled artisan would undoubtedly understand and expect that a multitude of sequences structurally related to SEQ ID NO:474, *e.g.*, sequences having at least 90% identity to SEQ ID NO:474, would be diagnostically useful in the same capacity as the specific species of SEQ ID NO:474. More particularly, sequences having at least 90% identity with SEQ ID NO:474, based upon their structural similarity to, and thus specificity for, a sequence of SEQ ID NO:474, will hybridize, using assays known in the art and described in the specification, to a sequence of SEQ ID NO:474, and accordingly would be useful in detecting over-expression of SEQ ID NO:474 in a biological sample in the same manner as one would use the precise sequence of SEQ ID NO:474 to detect over expression of SEQ ID NO:474 in a biological sample. This understanding and expectation on the part of the skilled artisan is soundly based upon fundamental scientific principles of nucleic acid hybridization, namely that a sequence having at least 90% identity to a sequence of SEQ ID NO:474 will indeed hybridize to the sequence of SEQ ID NO:474 and therefore will be useful in detecting cancers associated with over-expression of SEQ ID NO:474, despite the fact that the sequences are not identical with SEQ ID NO:474.

Moreover, by the present amendment, Applicants specifically incorporated this illustrative identifying characteristic into the claims under consideration, such that a polynucleotide of the invention is one that is "useful in the detection of breast cancer." Accordingly, in view of the applicants' identifying characteristic disclosed for SEQ ID NO:474, applicants respectfully submit that the skilled artisan would appreciate that applicants were in clear possession of a genus of sequences related by % identity to SEQ ID NO:474 that would be similarly useful in a diagnostic context based upon their

specificity for the sequence of SEQ ID NO:474. Applicants thus submit that the instant claims fully comply with the written description requirements of 35 U.S.C. § 112, first paragraph. Reconsideration and withdrawal of the rejection is respectfully requested.

With respect to the claimed isolated polynucleotide comprising at least the open reading frame of SEQ ID NO:474 reading on a full chromosome, Applicants submit that the specification defines "polynucleotide" on page 28, lines 22-26 as follows:

> As used herein, the terms "DNA segment" and "polynucleotide" refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. Therefore, a DNA segment encoding a polypeptide refers to a DNA segment that contains one or more coding sequences yet is substantially isolated away from, or purified free from, total genomic DNA of the species from which the DNA segment is obtained.

Further, the specification defines "isolated" on page 29, lines 6 – 11 as follows:

> "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA segment does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA segment as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

Moreover, the claimed invention centers on Applicants' discovery of numerous isoforms of the B726P breast tumor gene, more particularly on the full-length polynucleotide set forth in SEQ ID NO:474, that includes the coding region of one of these isoforms and that is over expressed in breast tumors as compared to normal breast and other normal tissues. Therefore, Applicants respectfully submit that they are entitled to open comprising language as recited in the claims. Additionally, Applicants respectfully submit that the specification clearly describes the open reading frame (*i.e.*, coding region) of SEQ ID NO:474, for example, in the sequence listing as the amino acid

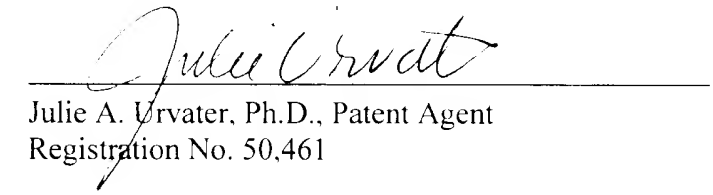
sequence set forth in SEQ ID NO:475, or on page 122, lines 14 – 18. Thus, it is urged that the pending claims fully satisfy the written description requirement of 35 U.S.C. § 112, first paragraph, and that the rejection of the claims may be properly withdrawn.

Favorable reconsideration and allowance of the pending claims are respectfully requested. The Examiner is invited to contact the undersigned with any questions, concerns or suggestions pertaining to this communication.

Respectfully submitted,

Yuqiu Jiang et al.

Seed Intellectual Property Law Group PLLC



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VERSION WITH MARKINGS TO SHOW CHANGES

In the claims:

Claims 1-3, 13-16, 21-38, 40-43, 48-76 have been cancelled.

Claim 80 has been canceled and replaced by newly rewritten claims 85-89.

Claim 6 has been amended as follows:

6. (Twice Amended) An isolated polynucleotide comprising at least the ~~coding region~~open reading frame of a sequence recited in SEQ ID NO:474.

81. (Amended) An expression vector comprising a polynucleotide of any one of claims 6 ~~or claim 80~~ and claims 85-89 operably linked to an expression control element.

82. (Amended) A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component comprising a polynucleotide according to any one of claims 6 and claims 85-89~~or claim 80~~.